

Abstract of Priority Documents

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TI Detecting multiple groups such as kinases or kinase substrates in test sample, comprises separating proteins in sample to produce one-dimensional array, contacting array with antibodies and detecting antibodies bound to groups.

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CA 2290335 A1 20010519 (200141) EN C12Q001-48

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NOVELTY - Detecting (M) multiple groups such as kinases or kinase substrates in a test sample comprising:

(1) electrophoretically separating proteins in the sample to produce a one-dimensional array of proteins so separated;

(2) contacting the array with antibodies such as anti-kinase (substrate) antibodies; and

(3) detecting the presence of antibodies bound to kinase (substrate) groups in the array, is new.

USE - (M) is useful for detecting multiple groups such as kinases or kinase substrates in a test sample (claimed). (M) is useful for the discovery of new protein kinases, to detect unknown proteins which can cross-react with kinase-specific antibodies, and to identify known proteins and detect new proteins that may bind with high affinity to a target protein.

ADVANTAGE - (M) has many advantages over standard 2-dimensional (2D) gel proteomic methods. (M) can be applied to any cell or tissue samples, and no prelabeling with radioisotopes is necessary, because kinase detection is based on immunoreactivity. (M) can be adapted for wide scale diagnostic applications because patterns of protein kinase expression are stable for periods of up to six hours before an organ is subjected to fractionation and freezing, providing the organ is stored during this time over ice. This procedure may be carried out within two days from start to finish when compared to the 2D gel electrophoresis which is extremely laborious, much more difficult to render and takes at least twice a time. (M) provides ability to compare multiple samples side by side, whereas the 2D gel can be used for a single sample. An advantage of (M) over other methods to examine protein-protein interactions such as the yeast two-hybrid method, is that it can detect interactions that are affected by the state of post-translation regulation of these proteins, such as their phosphorylation state.

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